

AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph 100 on page 31 with the following:

PCR. The RepeatMasker2 program (**available at <http://ftp.genome.washington.edu>**) was used to identify human repeat DNA sequences. Primers were designed to amplify unique sequences and repeat elements other than LINE as confirmed by a negative female control, yielding amplicons 300-500 bp in length. All primers had a uniform annealing temperature, which allowed a single PCR protocol to be used. It comprised an initial denaturation at 95°C for 10 min to activate AmpliTaq Gold[®], 14 cycles of denaturation at 94°C for 20s, primer annealing at 63-56°C using 0.5°C decrements, and extension at 72°C for 1 min, followed by 20 cycles at 94°C for 20 s, 56°C for 1 min, and 72°C for 1 min, and a final 5-min extension at 72°C. Each 50- μ l PCR reaction contained 1 U of AmpliTaq Gold[®] polymerase, 10 mM Tris-HCl, pH 8.3, 50 mM KCl, 2.5 mM MgCl₂, 0.1 mM each of the four deoxyribonucleotide triphosphates, 0.2 μ M each of forward/reverse primers, and 50 ng of genomic DNA. PCR yields were determined semi-quantitatively on ethidium bromide stained agarose gels.

Please replace paragraph 101 bridging pages 31 and 32 with the following:

DHPLC analysis. Unpurified PCR products were mixed at an equimolar ratio with a reference Y chromosome and subjected to a 3-minute 95°C denaturing step followed by gradual reannealing from 95 to 65°C over 30 min. Ten microliters of each mixture were loaded onto a DNASep[™] column (Transgenomic, San Jose, CA), and the amplicons were eluted in 0.1 M triethylammonium acetate, pH 7, with a linear acetonitrile gradient at a flow rate of 0.9 ml/min². Under appropriate temperature conditions, which were optimized by computer simulation (available at <http://insertion.stanford.edu/melt.html>), mismatches were recognized by the appearance of two or more peaks in the elution profiles.